

SEQUENCE LISTING

<110> Reed, John C.

<120> Novel Card Proteins Involved in Cell Death Regulation

<130> P-LJ 3650

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<170> PatentIn Ver. 2.0

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<211> 4422

<212> DNA

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Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
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Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
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Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
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Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
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Arg	Gly	Gln	Leu	Tyr	Gly	Asp	Arg	Phe	Gln	His	Val	Phe	Tyr	Phe	Ser	
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Cys	Arg	Glu	Leu	Ala	Gln	Ser	Lys	Val	Val	Ser	Leu	Ala	Glu	Leu	Ile	
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Arg	Pro	Glu	Arg	Leu	Leu	Phe	Ile	Leu	Asp	Gly	Val	Asp	Glu	Pro	Gly	
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Trp	Val	Leu	Gln	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu	His	Trp	Ser	Gln	
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Pro	Gln	Pro	Ala	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu	Gly	Lys	Thr	Ile	
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Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln	
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Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp	
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 580 585 590

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 Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
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 1265 1270 1275 1280

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His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
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Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
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Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
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Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
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Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
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Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
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Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
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Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
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Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
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Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
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Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
 370 375 380

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Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
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 465 470 475 480

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Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
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Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
565 570 575

Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
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Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
595 600 605

Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
610 615 620

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Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr
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Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
675 680 685

Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val
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Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His
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Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala
725 730 735

His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
740 745 750

Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
755 760 765

Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val
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785 790 795 800

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Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser
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Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser
980 985 990

His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe
995 1000 1005

Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val
1010 1015 1020

Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr
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Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val
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Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe
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Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val
1075 1080 1085

Met Arg Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln
1090 1095 1100

Phe Leu Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro
1105 1110 1115 1120

Leu Leu Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu
1125 1130 1135

Pro His Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe
1140 1145 1150

Gln Met Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala
1155 1160 1165

Arg Val Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro
1170 1175 1180

Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro
1185 1190 1195 1200

Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val
1205 1210 1215

Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu
1220 1225 1230

Leu Glu Leu Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu
1235 1240 1245

Phe Tyr Val Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp
1250 1255 1260

Lys Lys Asp Glu Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp
1265 1270 1275 1280

Leu Met Pro Ala Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro
1285 1290 1295

Ser Pro Leu Asp Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg
1300 1305 1310

Glu Gln Leu Ile Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys
 1315 1320 1325

Leu His Gly Gln Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala
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Glu Asn Thr Arg Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln
 345 1350 1355 1360

Ser Trp Asp Arg Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu
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Gly Leu Leu Pro Leu Ser Ser
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 1 5 10 15

aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg 96
 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
 20 25 30

cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg 144
 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
 35 40 45

agt ggc atg gag gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag 192
 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
 50 55 60

cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg 240
 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg

65	70	75	80	
tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc				288
Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe				
	85	90	95	
ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc				336
Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr				
	100	105	110	
tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc				384
Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys				
	115	120	125	
acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct				432
Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser				
	130	135	140	
gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt				480
Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu				
	145	150	155	160
cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc				528
Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala				
	165	170	175	
ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc				576
Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro				
	180	185	190	
agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg				624
Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu				
	195	200	205	
gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga				672
Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg				
	210	215	220	
gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg				720
Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr				
	225	230	235	240
ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag				768
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu				
	245	250	255	
cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag				816
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu				

260	265	270	
gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac			864
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His			
275	280	285	
ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg			912
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val			
290	295	300	
gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca			960
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro			
305	310	315	320
ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct			1008
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala			
325	330	335	
gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg			1056
Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly			
340	345	350	
aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc			1104
Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser			
355	360	365	
tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc			1152
Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile			
370	375	380	
gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct			1200
Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser			
385	390	395	400
agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga			1248
Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly			
405	410	415	
tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag			1296
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln			
420	425	430	
cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata			1344
Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile			
435	440	445	
ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag			1392
Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln			

450

455

460

aac ctc att cct tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg 1440
 Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
 465 470 475 480

ttc tct gag tcc agc agg aag gaa tat ttc tac aga tat ttc aca gat 1488
 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
 485 490 495

gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag 1536
 Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu
 500 505 510

ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act 1584
 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr
 515 520 525

tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc 1632
 Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
 530 535 540

aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa 1680
 Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
 545 550 555 560

gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct 1728
 Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
 565 570 575

gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg 1776
 Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
 580 585 590

aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt 1824
 Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
 595 600 605

att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc 1872
 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
 610 615 620

tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag 1920
 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
 625 630 635 640

aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg 1968
 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr

645	650	655	
cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt			2016
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg			
660	665	670	
ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac			2064
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn			
675	680	685	
atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc			2112
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val			
690	695	700	
ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac			2160
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His			
705	710	715	720
tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc			2208
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala			
725	730	735	
cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta			2256
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu			
740	745	750	
gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag			2304
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln			
755	760	765	
ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta			2352
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val			
770	775	780	
gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc			2400
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu			
785	790	795	800
ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt			2448
Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser			
805	810	815	
gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg			2496
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu			
820	825	830	
aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc			2544
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly			

835

840

845

ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac 2592
 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
 850 855 860

cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct 2640
 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
 865 870 875 880

gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta 2688
 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
 885 890 895

cag cga ctg cag ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag 2736
 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
 900 905 910

gac ctg gcc tct gtg ctt agt gcc agc ccc agc ctg aag gag cta gac 2784
 Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp
 915 920 925

ctg cag cag aac aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag 2832
 Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu
 930 935 940

ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg aaa cca agt 2880
 Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Lys Pro Ser
 945 950 955 960

gtg atg acc cct act gag ggc ctg gat acg gga gag atg agt aat agc 2928
 Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser
 965 970 975

aca tcc tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc 2976
 Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser
 980 985 990

cat gtt gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc 3024
 His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe
 995 1000 1005

cca att gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg 3072
 Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val
 1010 1015 1020

gaa ctc ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg 3120
 Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr

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aag cct ttg ggg act gac gat gac ttc tgg ggc ccc acg ggg cct gtg				3168
Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val				
	1045	1050	1055	
gct act gag gta gtt gac aaa gaa aag aac ttg tac cga gtt cac ttc				3216
Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe				
	1060	1065	1070	
cct gta gct ggc tcc tac cgc tgg ccc aac acg ggt ctc tgc ttt gtg				3264
Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val				
	1075	1080	1085	
atg aga gaa gcg gtg acc gtt gag att gaa ttc tgt gtg tgg gac cag				3312
Met Arg Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln				
	1090	1095	1100	
ttc ctg ggt gag atc aac cca cag cac agc tgg atg gtg gca ggg cct				3360
Phe Leu Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro				
	1105	1110	1115	1120
ctg ctg gac atc aag gct gag cct gga gct gtg gaa gct gtg cac ctc				3408
Leu Leu Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu				
	1125	1130	1135	
cct cac ttt gtg gct ctc caa ggg ggc cat gtg gac aca tcc ctg ttc				3456
Pro His Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe				
	1140	1145	1150	
caa atg gcc cac ttt aaa gag gag ggg atg ctc ctg gag aag cca gcc				3504
Gln Met Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala				
	1155	1160	1165	
agg gtg gag ctg cat cac ata gtt ctg gaa aac ccc agc ttc tcc ccc				3552
Arg Val Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro				
	1170	1175	1180	
ttg gga gtc ctc ctg aaa atg atc cat aat gcc ctg cgc ttc att ccc				3600
Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro				
	1185	1190	1195	1200
gtc acc tct gtg gtg ttg ctt tac cac cgc gtc cat cct gag gaa gtc				3648
Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val				
	1205	1210	1215	
acc ttc cac ctc tac ctg atc cca agt gac tgc tcc att cgg aag gcc				3696
Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Ala				

1410

1415

1420

ctc att atg gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca 4320
 Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro
 1425 1430 1435 1440

ctc agc agc tga 4332
 Leu Ser Ser

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<211> 1443

<212> PRT

<213> Homo sapiens

<400> 6

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Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
 20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
 35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
 50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
 65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
 85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
 100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
 115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
 130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
 145 150 155 160

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
 165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
 180 185 190

Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
 195 200 205

Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
 210 215 220

Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
 225 230 235 240

Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
 245 250 255

Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
 260 265 270

Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
 275 280 285

Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
 290 295 300

Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
 305 310 315 320

Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
 325 330 335

Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
 340 345 350

Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
 355 360 365

Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
 370 375 380

Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
 385 390 395 400

Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
 405 410 415

Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
 420 425 430

Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
 435 440 445
 Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln
 450 455 460
 Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
 465 470 475 480
 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
 485 490 495
 Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu
 500 505 510
 Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr
 515 520 525
 Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
 530 535 540
 Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
 545 550 555 560
 Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
 565 570 575
 Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
 580 585 590
 Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
 595 600 605
 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
 610 615 620
 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
 625 630 635 640
 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr
 645 650 655
 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg
 660 665 670
 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
 675 680 685

Ile	Phe	His	Cys	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	690	695	700	
Pro	Ser	Leu	Gln	Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His	705	710	715	720
Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	725	730	735	
His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	740	745	750	
Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	755	760	765	
Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	770	775	780	
Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	785	790	795	800
Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	805	810	815	
Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	820	825	830	
Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	835	840	845	
Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	850	855	860	
Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	865	870	875	880
Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	885	890	895	
Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	900	905	910	
Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	915	920	925	
Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	930	935	940	

Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Lys Pro Ser
 945 950 955 960

Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser
 965 970 975

Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser
 980 985 990

His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe
 995 1000 1005

Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val
 1010 1015 1020

Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr
 1025 1030 1035 1040

Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val
 1045 1050 1055

Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe
 1060 1065 1070

Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val
 1075 1080 1085

Met Arg Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln
 1090 1095 1100

Phe Leu Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro
 1105 1110 1115 1120

Leu Leu Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu
 1125 1130 1135

Pro His Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe
 1140 1145 1150

Gln Met Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala
 1155 1160 1165

Arg Val Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro
 1170 1175 1180

Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro
 1185 1190 1195 1200

Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val
 1205 1210 1215
 Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Ala
 1220 1225 1230
 Ile Asp Asp Leu Glu Met Lys Phe Gln Phe Val Arg Ile His Lys Pro
 1235 1240 1245
 Pro Pro Leu Thr Pro Leu Tyr Met Gly Cys Arg Tyr Thr Val Ser Gly
 1250 1255 1260
 Ser Gly Ser Gly Met Leu Glu Ile Leu Pro Lys Glu Leu Glu Leu Cys
 1265 1270 1275 1280
 Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly
 1285 1290 1295
 His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys Asp Glu
 1300 1305 1310
 Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala
 1315 1320 1325
 Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp
 1330 1335 1340
 Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile
 1345 1350 1355 1360
 Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln
 1365 1370 1375
 Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg
 1380 1385 1390
 Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg
 1395 1400 1405
 Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His
 1410 1415 1420
 Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro
 1425 1430 1435 1440
 Leu Ser Ser

<210> 7
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1296)

<400> 7

atg atg aga cag agg cag agc cat tat tgt tcc gtg ctg ttc ctg agt	48
Met Met Arg Gln Arg Gln Ser His Tyr Cys Ser Val Leu Phe Leu Ser	
1 5 10 15	
gtc aac tat ctg ggg ggg aca ttc cca gga gac att tgc tca gaa gag	96
Val Asn Tyr Leu Gly Gly Thr Phe Pro Gly Asp Ile Cys Ser Glu Glu	
20 25 30	
aat caa ata gtt tcc tct tat gct tct aaa gtc tgt ttt gag atc gaa	144
Asn Gln Ile Val Ser Ser Tyr Ala Ser Lys Val Cys Phe Glu Ile Glu	
35 40 45	
gaa gat tat aaa aat cgt cag ttt ctg ggg cct gaa gga aat gtg gat	192
Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu Gly Asn Val Asp	
50 55 60	
gtt gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc ccc	240
Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro	
65 70 75 80	
act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg gta	288
Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val	
85 90 95	
agg gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag cac	336
Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His	
100 105 110	
ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc ccc	384
Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro	
115 120 125	
ttg ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc cac	432
Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His	
130 135 140	
ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg ttt	480

[illegible]

Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His
 340 345 350

cgg caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat gat 1104
 Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp
 355 360 365

ctc cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg gag 1152
 Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu
 370 375 380

cag gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg gtg 1200
 Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val
 385 390 395 400

gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att agt 1248
 Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser
 405 410 415

gaa agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg taa 1296
 Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu
 420 425 430

aatgagtcag ttaggtagtc tggaagagag aatccagcgt tctcattgga aatggataaa 1356

cagaaatgtg atcattgatt tcagtgttca agacagaaga agactgggta acatctatca 1416

cacaggcttt caggacagac ttgtaacctg gcatgtacct attgactgta tcctcatgca 1476

ttttcctcaa g 1487

<210> 8

<211> 431

<212> PRT

<213> Homo sapiens

<400> 8

Met Met Arg Gln Arg Gln Ser His Tyr Cys Ser Val Leu Phe Leu Ser
 1 5 10 15

Val Asn Tyr Leu Gly Gly Thr Phe Pro Gly Asp Ile Cys Ser Glu Glu
 20 25 30

Asn Gln Ile Val Ser Ser Tyr Ala Ser Lys Val Cys Phe Glu Ile Glu
 35 40 45

Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu Gly Asn Val Asp

50	55	60
Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro		
65	70	75 80
Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val		
	85	90 95
Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His		
	100	105 110
Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro		
	115	120 125
Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His		
	130	135 140
Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe		
	145	150 155 160
Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala		
	165	170 175
Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu		
	180	185 190
Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro		
	195	200 205
Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile		
	210	215 220
Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala		
	225	230 235 240
Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser		
	245	250 255
Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn		
	260	265 270
Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg		
	275	280 285
Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met		
	290	295 300
Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu		

305		310		315		320
Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala						
	325		330		335	
Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His						
	340		345		350	
Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp						
	355		360		365	
Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu						
	370		375		380	
Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val						
385		390		395		400
Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser						
	405		410		415	
Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu						
	420		425		430	

<210> 9

<211> 4556

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(4365)

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 9

atg gct ggc gga gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg	48
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu	
1 5 10 15	

aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg	96
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala	
20 25 30	

cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg	144
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr	

225	230	235	240	
ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag				768
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu				
	245	250	255	
cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag				816
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu				
	260	265	270	
gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac				864
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His				
	275	280	285	
ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg				912
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val				
	290	295	300	
gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca				960
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro				
305	310	315	320	
ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct				1008
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala				
	325	330	335	
gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg				1056
Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly				
	340	345	350	
aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc				1104
Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser				
	355	360	365	
tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc				1152
Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile				
	370	375	380	
gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct				1200
Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser				
385	390	395	400	
agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga				1248
Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly				
	405	410	415	
tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag				1296
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln				

610	615	620	
tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag			1920
Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu			
625	630	635	640
aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg			1968
Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr			
	645	650	655
cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt			2016
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg			
	660	665	670
ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac			2064
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn			
	675	680	685
atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc			2112
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val			
	690	695	700
ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac			2160
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His			
705	710	715	720
tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc			2208
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala			
	725	730	735
cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta			2256
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu			
	740	745	750
gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag			2304
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln			
	755	760	765
ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta			2352
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val			
	770	775	780
gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc			2400
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu			
785	790	795	800
ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt			2448
Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser			

805	810	815	
gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg			2496
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu			
820	825	830	
aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc			2544
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly			
835	840	845	
ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac			2592
Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn			
850	855	860	
cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct			2640
Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala			
865	870	875	880
gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta			2688
Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu			
885	890	895	
cag cga ctg cag ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag			2736
Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln			
900	905	910	
gac ctg gcc tct gtg ctt agt gcc agc ccc agc ctg aag gag cta gac			2784
Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp			
915	920	925	
ctg cag cag aac aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag			2832
Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu			
930	935	940	
ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag			2880
Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln			
945	950	955	960
aca act ctg agt gat gag atg agg cag gaa ctg agg gcc ctg gag cag			2928
Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln			
965	970	975	
gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg			2976
Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met			
980	985	990	
acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc			3024
Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser			

995	1000	1005	
tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt			3072
Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val			
1010	1015	1020	
gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att			3120
Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile			
1025	1030	1035	1040
gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc			3168
Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu			
1045	1050	1055	
ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg aag cct			3216
Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro			
1060	1065	1070	
ttg ggg act gac gat gac ttt ctg ggg cct gaa gga aat gtg gat gtt			3264
Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val Asp Val			
1075	1080	1085	
gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc ccc act			3312
Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro Thr			
1090	1095	1100	
gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg gta agg			3360
Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val Arg			
1105	1110	1115	1120
gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag cac ctg			3408
Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His Leu			
1125	1130	1135	
gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc ccc ttg			3456
Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro Leu			
1140	1145	1150	
ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc cac ctc			3504
Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His Leu			
1155	1160	1165	
ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg ttt ctc			3552
Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe Leu			
1170	1175	1180	
gtt gcc cat ttt aag aat gaa ggg atg gtc ctg gag cat cca gcc cgg			3600
Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala Arg			

1185	1190	1195	1200	
gtg gag cct ttc tat gct gtc ctg gaa agc ccc agc ttc tct ctg atg				3648
Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu Met				
1205		1210	1215	
ggc atc ctg ctg cgg atc gcc agt ggg act cgc ctc tcc atc ccc atc				3696
Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro Ile				
1220	1225		1230	
act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat att aag				3744
Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile Lys				
1235	1240		1245	
ttc cac ttg tac ctt gtc ccc agc gac gcc ttg cta aca aag gcg ata				3792
Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala Ile				
1250	1255		1260	
gat gat gag gaa gat cgc ttc cat ggt gtg cgc ctg cag act tcg ccc				3840
Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser Pro				
1265	1270	1275	1280	
cca atg gaa ccc ctg aac ttt ggt tcc agt tat att gtg tct aat tct				3888
Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn Ser				
1285	1290		1295	
gct aac ctg aaa gta atg ccc aag gag ttg aaa ttg tcc tac agg agc				3936
Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg Ser				
1300	1305		1310	
cct gga gaa att cag cac ttc tca aaa ttc tat gct ggg cag atg aag				3984
Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met Lys				
1315	1320		1325	
gaa ccc att caa ctt gag att act gaa aaa aga cat ggg act ttg gtg				4032
Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu Val				
1330	1335		1340	
tgg gat act gag gtg aag cca gtg gat ctc cag ctt gta gct gca tca				4080
Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala Ser				
1345	1350	1355	1360	
gcc cct cct cct ttc tca ggt gca gcc ttt gtg aag gag aac cac cgg				4128
Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His Arg				
1365	1370		1375	
caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat gat ctc				4176
Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp Leu				

1380	1385	1390	
cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg gag cag			4224
Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu Gln			
1395	1400	1405	
gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg gtg gag			4272
Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val Glu			
1410	1415	1420	
aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att agt gaa			4320
Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser Glu			
1425	1430	1435	1440
agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg taa			4365
Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu			
1445	1450	1455	
aatgagtcag ttaggtagtc tggaagagag aatccagcgt tctcattgga aatggataaa 4425			
cagaaatgtg atcattgatt tcagtgttca agacagaaga agactgggta acatctatca 4485			
cacaggcttt caggacagac ttgtaacctg gcatgtacct attgactgta tcctcatgca 4545			
ttttcctcaa g 4556			
<210> 10			
<211> 1454			
<212> PRT			
<213> Artificial Sequence			
<400> 10			
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu			
1	5	10	15
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala			
20	25	30	
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr			
35	40	45	
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln			
50	55	60	
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg			
65	70	75	80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
145 150 155 160

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
180 185 190

Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
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Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
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Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
225 230 235 240

Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
245 250 255

Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
260 265 270

Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
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Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
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Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
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Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
325 330 335

Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
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Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
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Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
 370 375 380

Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
 385 390 395 400

Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
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Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
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Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
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Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln
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Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
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Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
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Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu
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Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr
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Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
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Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
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Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
 565 570 575

Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
 580 585 590

Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
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 Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
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 Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
 625 630 635 640
 Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr
 645 650 655
 Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg
 660 665 670
 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
 675 680 685
 Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val
 690 695 700
 Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His
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 Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala
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 His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
 740 745 750
 Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
 755 760 765
 Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val
 770 775 780
 Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu
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 Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser
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 Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu
 820 825 830
 Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly
 835 840 845

Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
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Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
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Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
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Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
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Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp
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Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu
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Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln
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Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln
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Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
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Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
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Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile
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Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu
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Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val Arg
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 Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His Leu
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 Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His Leu
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 Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe Leu
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 Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala Arg
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 Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu Met
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 Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn Ser
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 Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg Ser
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 Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met Lys
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 Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu Val
 1330 1335 1340
 Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala Ser
 1345 1350 1355 1360

Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His Arg
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Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp Leu
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Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu Gln
1395 1400 1405

Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val Glu
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<220>

<223> Description of Artificial Sequence: Synthetic
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Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
20 25 30

cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg 144
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
35 40 45

agt ggc atg gag gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag 192
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
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cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg	240
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg	
65 70 75 80	
tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc	288
Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe	
85 90 95	
ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc	336
Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr	
100 105 110	
tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc	384
Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
115 120 125	
acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct	432
Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
130 135 140	
gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt	480
Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu	
145 150 155 160	
cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc	528
Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala	
165 170 175	
ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc	576
Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro	
180 185 190	
agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg	624
Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu	
195 200 205	
gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga	672
Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg	
210 215 220	
gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg	720
Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr	
225 230 235 240	
ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag	768
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu	
245 250 255	

cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag	816
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu	
260 265 270	
gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac	864
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His	
275 280 285	
ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg	912
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val	
290 295 300	
gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca	960
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro	
305 310 315 320	
ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct	1008
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala	
325 330 335	
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Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly	
340 345 350	
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Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser	
355 360 365	
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Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile	
370 375 380	
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Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser	
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Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly	
405 410 415	
tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag	1296
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln	
420 425 430	
cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata	1344
Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile	
435 440 445	

ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag	1392
Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln	
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Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly	
465 470 475 480	
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Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp	
485 490 495	
gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag	1536
Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu	
500 505 510	
ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act	1584
Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr	
515 520 525	
tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc	1632
Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser	
530 535 540	
aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa	1680
Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln	
545 550 555 560	
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Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala	
565 570 575	
gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg	1776
Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg	
580 585 590	
aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt	1824
Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly	
595 600 605	
att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc	1872
Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu	
610 615 620	
tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag	1920
Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu	
625 630 635 640	

aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg	1968
Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr	
645 650 655	
cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt	2016
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg	
660 665 670	
ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac	2064
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn	
675 680 685	
atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc	2112
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val	
690 695 700	
ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac	2160
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His	
705 710 715 720	
tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc	2208
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala	
725 730 735	
cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta	2256
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu	
740 745 750	
gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag	2304
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln	
755 760 765	
ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta	2352
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val	
770 775 780	
gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc	2400
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu	
785 790 795 800	
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Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser	
805 810 815	
gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg	2496
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu	
820 825 830	

aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc	2544
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly	
835 840 845	
ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac	2592
Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn	
850 855 860	
cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct	2640
Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala	
865 870 875 880	
gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta	2688
Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu	
885 890 895	
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Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln	
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gac ctg gcc tct gtg ctt agt gcc agc ccc agc ctg aag gag cta gac	2784
Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp	
915 920 925	
ctg cag cag aac aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag	2832
Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu	
930 935 940	
ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg aaa cca agt	2880
Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Lys Pro Ser	
945 950 955 960	
gtg atg acc cct act gag ggc ctg gat acg gga gag atg agt aat agc	2928
Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser	
965 970 975	
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Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser	
980 985 990	
cat gtt gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc	3024
His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe	
995 1000 1005	
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Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val	
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Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr	
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Lys Pro Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val	
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gat gtt gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc	3216
Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe	
1060 1065 1070	
ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg	3264
Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu	
1075 1080 1085	
gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag	3312
Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln	
1090 1095 1100	
cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc	3360
His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly	
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Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile	
1125 1130 1135	
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His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp	
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ccc atc act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat	3648
Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp	
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Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys	
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Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr	
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Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser	
1250 1255 1260	
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Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr	
1265 1270 1275 1280	
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Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln	
1285 1290 1295	
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Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr	
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Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala	
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His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp	
1345 1350 1355 1360	
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Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val	
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1380 1385 1390	
gtg gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att	4224
Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile	
1395 1400 1405	

agt gaa agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg 4272
 Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu
 1410 1415 1420

taa aatgagtcag ttaggtagtc tggaagagag aatccagcgt tctcattgga 4325
 1425

aatggataaa cagaaatgtg atcattgatt tcagtgttca agacagaaga agactgggta 4385

acatctatca cacaggcttt caggacagac ttgtaacctg gcatgtacct attgactgta 4445

tcctcatgca ttttcctcaa g 4466

<210> 12

<211> 1424

<212> PRT

<213> Artificial Sequence

<400> 12

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
 1 5 10 15

Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
 20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
 35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
 50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
 65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
 85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
 100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
 115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
 130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
 145 150 155 160
 Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
 165 170 175
 Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
 180 185 190
 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
 195 200 205
 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
 210 215 220
 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
 225 230 235 240
 Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
 245 250 255
 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
 260 265 270
 Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
 275 280 285
 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
 290 295 300
 Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
 305 310 315 320
 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
 325 330 335
 Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
 340 345 350
 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
 355 360 365
 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
 370 375 380
 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
 385 390 395 400

Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
 405 410 415

Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
 420 425 430

Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
 435 440 445

Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln
 450 455 460

Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
 465 470 475 480

Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
 485 490 495

Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu
 500 505 510

Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr
 515 520 525

Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser
 530 535 540

Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
 545 550 555 560

Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala
 565 570 575

Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
 580 585 590

Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
 595 600 605

Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
 610 615 620

Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
 625 630 635 640

Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr
 645 650 655

Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg
 660 665 670
 Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn
 675 680 685
 Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val
 690 695 700
 Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His
 705 710 715 720
 Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala
 725 730 735
 His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
 740 745 750
 Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
 755 760 765
 Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val
 770 775 780
 Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu
 785 790 795 800
 Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser
 805 810 815
 Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu
 820 825 830
 Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly
 835 840 845
 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
 850 855 860
 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
 865 870 875 880
 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
 885 890 895
 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
 900 905 910

Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp
 915 920 925

Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu
 930 935 940

Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Lys Pro Ser
 945 950 955 960

Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser
 965 970 975

Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser
 980 985 990

His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe
 995 1000 1005

Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val
 1010 1015 1020

Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr
 1025 1030 1035 1040

Lys Pro Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val
 1045 1050 1055

Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe
 1060 1065 1070

Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu
 1075 1080 1085

Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln
 1090 1095 1100

His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly
 1105 1110 1115 1120

Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile
 1125 1130 1135

His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp
 1140 1145 1150

Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro
 1155 1160 1165

Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser			
1170	1175	1180	
Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile			
185	1190	1195	1200
Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp			
	1205	1210	1215
Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys			
	1220	1225	1230
Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr			
	1235	1240	1245
Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser			
	1250	1255	1260
Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr			
265	1270	1275	1280
Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln			
	1285	1290	1295
Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr			
	1300	1305	1310
Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala			
	1315	1320	1325
Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn			
	1330	1335	1340
His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp			
345	1350	1355	1360
Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val			
	1365	1370	1375
Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met			
	1380	1385	1390
Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile			
	1395	1400	1405
Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu			
1410	1415	1420	

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
ccgaattcac catggctggc ggagcctggg gc 32

<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ccgctcgagt caacagaggg ttgtggtggt cttg 34

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
cccgaattcg aacctcgcat agtcatactg c 31

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gtcccacaac agaattcaat ctcaacggtc 30

<210> 17
<211> 21
<212> DNA
<213> Homo sapiens

<400> 17
tgtgatgaga gaagcgggtga c

21

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
ccgctcgagc aaagaagggt cagccaaagc

30

ccgctcgagc aaagaagggt cagccaaagc